Nucleotide and Amino Acid Sequence of AIM-I

```
        GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATG
-51     -+---------+---------+---------+---------+---------+-------    8
        CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATAC
-16                                                        M  A  M    3


        ATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACA
 9      -+---------+---------+---------+---------+---------+-------   68
        TACCTCCAGGTCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGT
 4       M  E  V  Q  G  G  P  S  L  G  Q  T  C  V  L  I  V  I  F  T   23


        GTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAG
 69     -+---------+---------+---------+---------+---------+-------   128
        CACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTC
 24      V  L  L  Q  S  L  C  V  A  V  T  Y  V  Y  F  T  N  E  L  K   43


        CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
 129    -+---------+---------+---------+---------+---------+-------   188
        GTCTACGTCCTGTTCATGAGGTTTTCACCGTAACGAACAAAGAATTTTCTTCTACTGTCA
 44      Q  M  Q  D  K  Y  S  K  S  G  I  A  C  F  L  K  E  D  D  S   63


        TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
 189    -+---------+---------+---------+---------+---------+-------   248
        ATAACCCTGGGGTTACTGCTTCTCTCATACTTGTCGGGGACGACCGTTCAGTTCACCGTT
 64      Y  W  D  P  N  D  E  E  S  M  N  S  P  C  W  Q  V  K  W  Q   83


        CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
 249    -+---------+---------+---------+---------+---------+-------   308
        GAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGGAGACTCCTTTGGTAAAGATGTCAA
 84      L  R  Q  L  V  R  K  M  I  L  R  T  S  E  E  T  I  S  T  V   103


        CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
 309    -+---------+---------+---------+---------+---------+-------   368
        GTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTCTCCAGGAGTCTCTCATCGT
 104     Q  E  K  Q  Q  N  I  S  P  L  V  R  E  R  G  P  Q  R  V  A   123


        GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
 369    -+---------+---------+---------+---------+---------+-------   428
        CGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTA
 124     A  H  I  T  G  T  R  G  R  S  N  T  L  S  S  P  N  S  K  N   143


        GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC
 429    -+---------+---------+---------+---------+---------+-------   488
        CTTTTCCGAGACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAG
 144     E  K  A  L  G  R  K  I  N  S  W  E  S  S  R  S  G  H  S  F   163
```

FIG.1A

```
           CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
489        -+---------+---------+---------+---------+---------+--------   548
           GACTCGTTGAACGTGAACTCCTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATG
164        L  S  N  L  H  L  R  N  G  E  L  V  I  H  E  K  G  F  Y  Y   183

           ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
549        -+---------+---------+---------+---------+---------+--------   608
           TAGATAAGGGTTTGTATGAAAGCTAAAGTCCTCCTTTATTTTCTTTTGTGTTTCTTGCTG
184        I  Y  S  Q  T  Y  F  R  F  Q  E  E  I  K  E  N  T  K  N  D   203

           AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
609        -+---------+---------+---------+---------+---------+--------   668
           TTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACTAC
204        K  Q  M  V  Q  Y  I  Y  K  Y  T  S  Y  P  D  P  I  L  L  M   223

           AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
669        -+---------+---------+---------+---------+---------+--------   728
           TTTTCACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA
224        K  S  A  R  N  S  C  W  S  K  D  A  E  Y  G  L  Y  S  I  Y   243

           CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
729        -+---------+---------+---------+---------+---------+--------   788
           GTTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC
244        Q  G  G  I  F  E  L  K  E  N  D  R  I  F  V  S  V  T  N  E   263

           CACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAACTG
789        -+---------+---------+---------+---------+---------+--------   848
           GTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAACCGATTGAC
264        H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V  G       281

           ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGATACACTA
849        -+---------+---------+---------+---------+---------+--------   908
           TGGACCTTTCTTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGAT

           TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAAC
909        -+---------+---------+---------+---------+---------+--------   968
           ACTTCTACAAAGTTTTTTAGACTGGTTTTGTTTGTTTGTCTTTTGTCTTTTGTTTTTTTG

           CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTG
969        -+---------+---------+---------+---------+---------+--------   1028
           GAGATACGTTAGACTCATCTCGTCGGTGTTGGTTTTTTAAGATGTTGTGTGTGACAAGAC

           AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCT
1029       -+---------+---------+---------+---------+---------+--------   1088
           TTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCCTGAGATGGA

           CATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGG
1089       -+---------+---------+---------+---------+---------+--------   1148
           GTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGTAATTACGTTACC
```

FIG.1B

```
        TTAACATCTTCTGTCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAGCGCAACAA
1149    -+---------+---------+---------+---------+---------+-------    1208
        AATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCGCGTTGTT

        TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATC
1209    -+---------+---------+---------+---------+---------+-------    1268
        AGGTAGAGAGTTCATCACATAGTGTCATCATCGGAGGTCCAAAGGAATTCCCTGTTGTAG

        CTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGC
1269    -+---------+---------+---------+---------+---------+-------    1328
        GAATTCAGTTTTCTCTCTTCTCCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACCG

        TCACACCTGTAATCCCAACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGA
1329    -+---------+---------+---------+---------+---------+-------    1388
        AGTGTGGACATTAGGGTTGTAAAACCCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCT

        TCAAGACCATAGTGACCAACATAGTGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGC
1389    -+---------+---------+---------+---------+---------+-------    1448
        AGTTCTGGTATCACTGGTTGTATCACTTTGGGGTAGAGATGACTTTCACGTTTTTAATCG

        TGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG
1449    -+---------+---------+---------+---------+---------+-------    1508
        ACCCACACAACCGTGTACGGACATCAGGGTCGATGAACTCTCCGACTCCGTCCTCTTAGC

        TTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG
1509    -+---------+---------+---------+---------+---------+-------    1568
        AAACTTGGGCCCTCCGTCTCCAACGTCACACCACTCTAGTACGGTGATGTGAGGTCGGAC

        GCGACAGAGCGAGACTTGGTTTC
1569    -+---------+---------+-     1591
        CGCTGTCTCGCTCTGAACCAAAG
```

FIG.1C

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 %   Identity = 22.892 %)

```
  4 MEVQGGPSLGQTCVLIVIFTVL................LQSLCVAVTYV 36
    ::  ::..::........::..  | :             |.. ..:....
 15 vdssasspwappgtvlpcptsvprrpgqrrpppppppppplppppppppplp 64

 37 YFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQ 86
    :.  |..:..: ..|. |:|      :     ::. . :| ::|..
 65 plp..lpplkkrgnhstglcllvm..ffmvlvalvglglgmfql.fhlqk 109

 87 LVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 136
    : .: .||:  ...  ||| . .. ..|: . | .||:|   |:||.
110 elaelrestsqmhtasslekqighpspppekkelrkvahlt...gksnsr 156

137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
    | | ..::.                | :||.:..:.|:|||:|.|:|::||
157 smplewedty............givllsgvkykkgglvinetglyfvys 193

187 QTYFRFQEEIKENTKNDKQMVQYIYKYTS.YPDPILLMKSARNSCWSKDA 235
    ..|||      :...  |: .: : :|. .| ||:.:::|.: . |: ...:.
194 kvyfr......gqscnnlplshkvymrnskypqdlvmmegkmmsycttgq 237

236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
    ::  | |  |::|:|...|:::|.|.:  |:::::....||| : :
238 mwar.ssylgavfnltsadhlyvnvselslvnfeesqtffglykl 281
```

FIG.2

Alignment Report of AIM-I, hFas Ligand, TNF-α and TNF-β
by Clustal Method with PAM250 Residue Weight Table

```
                   10              20              30
1   M A M M E V Q G G P S L - - - - - G Q T C V L I V I F T V L   AIM 1
1   M Q Q P M N Y P C P Q I F W V D S S A T S S W A P P G S V F   FAS LIGAND
1   M - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   tnfa.pep
1   M - - - - - - - - - - - - - - - - - - - - - T P P E R L F     tnfb.pep

                   40              50              60
26  L Q S L C V A V T Y V Y F T N E L K Q M Q D K Y S K S G I A   AIM 1
31  P C P S C G P R G - - - - P D Q R R P P P P P P P V S P L P   FAS LIGAND
2   - - - - - - - - - - - - - - - - - - - S T E S M I R D V E     tnfa.pep
9   L P R V C G T T - - - - - - - - - - - - - - - - - - - - - -   tnfb.pep

                   70              80              90
56  C F L K E D D S Y W D P N D E E S M N S P C W Q V K W Q L R   AIM 1
57  - - P P S Q P L P L P P L T P L K K K D H N T N L W L P V V   FAS LIGAND
12  - - L A E E A L P - - - - - - - K K T G G P Q G S R R C L     tnfa.pep
17  - - - - - - - - - - - - - - - - - - - - - - - L W L L         tnfb.pep

                   100             110             120
86  Q L V R K M I L R T S E E T I S T V Q E K Q Q N I S P L V R   AIM 1
85  F F M V L V A L V G M G L G - M Y Q L F H L Q K E L A E L R   FAS LIGAND
32  F L S L F S F L I V A G A T L F C L L H F G V I G P Q R E     tnfa.pep
21  L L G L L L V L - - - - - - - - - - - - - - - L P G A Q       tnfb.pep

                   130             140             150
116 E K G P Q R V A A H I T G T R G R S N T L S S P N S K N E K   AIM 1
114 E F T - N Q S L K V S S F E K Q I A N P S T P S E K K E P R   FAS LIGAND
62  E S P R D L S L I S P L A Q A V R S S S R T P S D - - - - K   tnfa.pep
34  G L P - G V G L T P S A A Q T A R Q H P K M H L A H S T L K   tnfb.pep

                   160             170             180
146 A L G R K I N S - - - - - - - - - W E S S R S G H S F L S N   AIM 1
143 S V A H L T G N P H S R S I P L E W E D T Y G T A L I - S G   FAS LIGAND
88  P V A H V V A N P Q A E G Q - L Q W L N R R A N A L L A N G   tnfa.pep
63  P A A H L I G D P - S K Q N S L L W R A N T D R A F L Q D C   tnfb.pep
```

FIG.3A

```
                       190              200              210
167  L H L R N G K L V I H E K G F Y Y I Y S Q T Y F R F Q E E I    AIM 1
172  V K Y K K G G L V I N E T G L Y F V Y S K V Y F R G Q S C N    FAS LIGAND
117  V E L R D N Q L V V P S E G L Y L I Y S Q V L F K G Q S C -    tnfa.pep
 92  F S L S N N S L L V P T S G I Y F V Y S Q V V F S C K A Y S    tnfb.pep

                       220              230              240
197  K E N T K N D K Q M V Q Y I Y K Y T S - Y P D P I L L M K S    AIM 1
202  N Q P - - - - - - L N H K V Y M R N S K Y P E D L V L M E E    FAS LIGAND
146  - - - P S T H V L L T H T I S R I A V S Y Q T K V N L L S A    tnfa.pep
122  P K A P S S P L Y L A H E V Q L F S S Q Y P F H V P L L S S    tnfb.pep

                       250              260              270
226  A R N S C W S K D A E Y G L - - - - - Y S I Y Q G G I F E L    AIM 1
226  K R L N Y C - - - - - - T T G Q I W A H S S Y L G A V F N L    FAS LIGAND
173  I K S P C Q R E T P E G A E A K P W Y E P I Y L G C V F Q L    tnfa.pep
152  Q K M V Y P - - - - - - G L Q E P W L H S M Y H G A A F Q L    tnfb.pep

                       280              290              300
251  K E N D R I F V S V T N E H L I D K D H E A S - F F G A F L    AIM 1
250  T S A D H L Y V N I S Q L S L I N F E E S - K T F F G L Y -    FAS LIGAND
203  E K G D R L S A E I N R P D Y L D F A E S G Q V Y F G I I -    tnfa.pep
176  T Q G D Q L S T R T D G I P H L V L S P S - T V F F G A F -    tnfb.pep


280  V G -                                                          AIM 1
278  - K L                                                          FAS LIGAND
232  - A L                                                          tnfa.pep
204  - A L                                                          tnfb.pep
```

Decoration 'Decoration #1': Box residues that match the
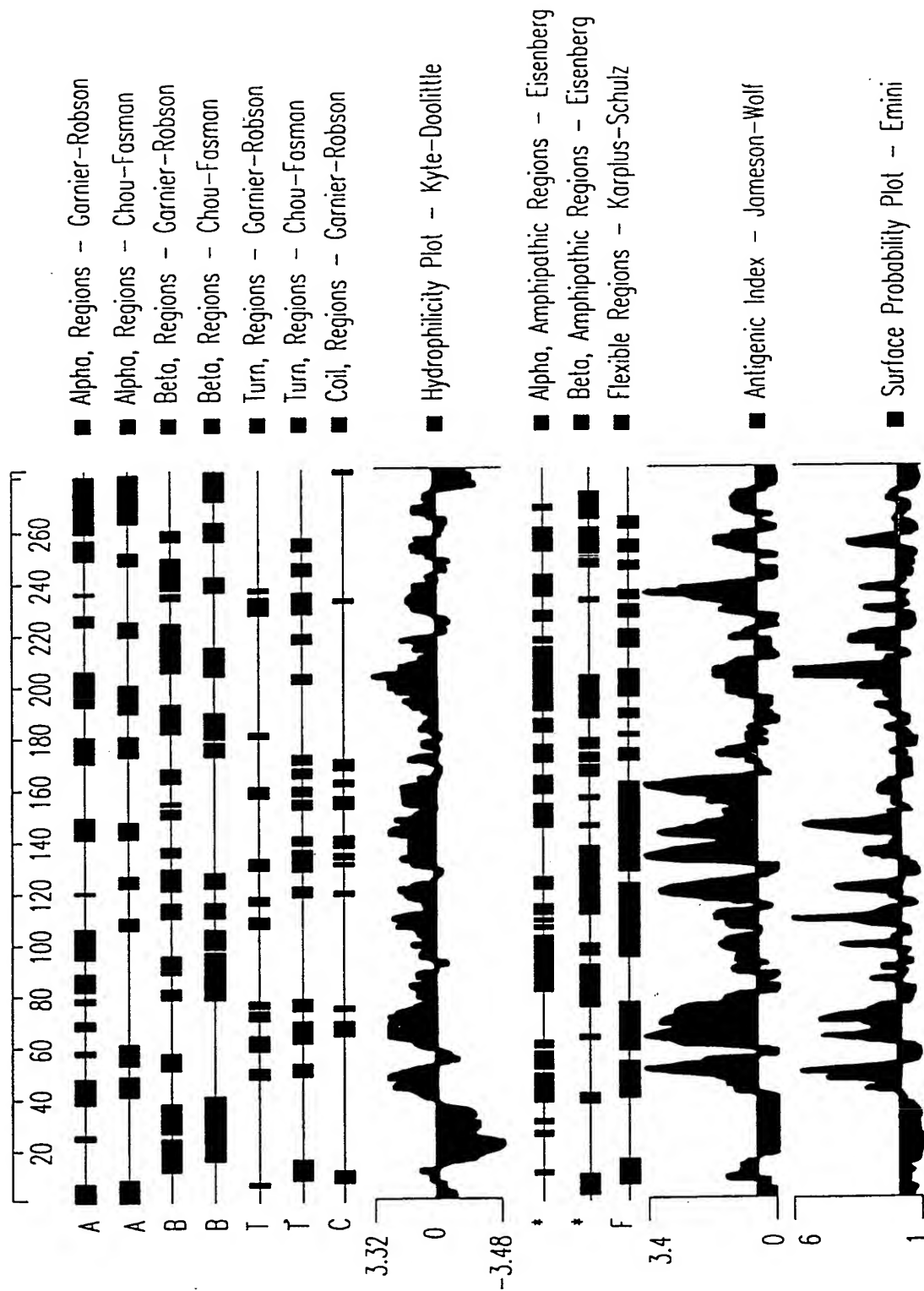Consensus within 2 distance units.

FIG.3B

REGIONAL ANALYSIS OF AIM-1 PROTEIN

- Alpha, Regions – Garnier–Robson
- Alpha, Regions – Chou–Fasman
- Beta, Regions – Garnier–Robson
- Beta, Regions – Chou–Fasman
- Turn, Regions – Garnier–Robson
- Turn, Regions – Chou–Fasman
- Coil, Regions – Garnier–Robson

- Hydrophilicity Plot – Kyte–Doolittle

- Alpha, Amphipathic Regions – Eisenberg
- Beta, Amphipathic Regions – Eisenberg
- Flexible Regions – Karplus–Schulz

- Antigenic Index – Jameson–Wolf

- Surface Probability Plot – Emini

FIG.4